

RAW SEQUENCE LISTING

EF5

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/555,735A
Source: 1 Fwd
Date Processed by STIC: 2/27/07

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 02/27/2007

PATENT APPLICATION: US/10/555,735A

TIME: 15:05:50

Input Set : N:\efs\02_27_07\10555735a_efs\INTM01901USseqlist2.txt

Output Set: N:\CRF4\02272007\J555735A.raw

```

4 <110> APPLICANT: Blatt, Lawrence M.
6 <120> TITLE OF INVENTION: SYNTHETIC CHEMOKINE RECEPTOR LIGANDS AND
7   METHODS OF USE THEREOF
9 <130> FILE REFERENCE: INTM-033WO
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/555,735A
C--> 12 <141> CURRENT FILING DATE: 2005-11-07
14 <150> PRIOR APPLICATION NUMBER: 60/471,404
15 <151> PRIOR FILING DATE: 2003-05-16
17 <160> NUMBER OF SEQ ID NOS: 20
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 77
23 <212> TYPE: PRT
24 <213> ORGANISM: Artificial Sequence
26 <220> FEATURE:
27 <223> OTHER INFORMATION: consensus IP-10 sequence
29 <400> SEQUENCE: 1
30 Val Pro Leu Ser Arg Thr Gly Arg Cys Thr Cys Ile Ser Ile Ser Asn
31 1           5           10           15
32 Gln Pro Val Asn Pro Arg Ser Leu Glu Lys Leu Glu Ile Ile Pro Pro
33           20           25           30
34 Ser Gln Phe Cys Pro Lys Ile Glu Ile Ile Ala Thr Leu Lys Lys Asn
35           35           40           45
36 Gly Glu Gln Arg Cys Leu Asn Pro Glu Ser Lys Ala Ile Lys Asn Leu
37           50           55           60
38 Ile Lys Lys Val Ser Arg Glu Met Ser Lys Lys Ser Pro
39 65           70           75
42 <210> SEQ ID NO: 2
43 <211> LENGTH: 74
44 <212> TYPE: PRT
45 <213> ORGANISM: Artificial Sequence
47 <220> FEATURE:
48 <223> OTHER INFORMATION: consensus I-TAC sequence
50 <400> SEQUENCE: 2
51 Phe Pro Met Phe Arg Arg Gly Arg Cys Leu Cys Ile Ser Pro Gly Val
52 1           5           10           15
53 Lys Ala Val Lys Val Ala Ser Leu Glu Lys Leu Ser Ile Met Tyr Pro
54           20           25           30
55 Ser Asn Asn Cys Asp Lys Ile Glu Ile Ile Ala Thr Leu Lys Lys Asn
56           35           40           45
57 Gly Gly Gln Arg Cys Leu Asn Pro Lys Ser Lys Gln Ala Lys Leu Leu
58           50           55           60
59 Ile Lys Lys Val Glu Arg Lys Lys Asn Phe

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60 65                               70
63 <210> SEQ ID NO: 3
64 <211> LENGTH: 104
65 <212> TYPE: PRT
66 <213> ORGANISM: Artificial Sequence
68 <220> FEATURE:
69 <223> OTHER INFORMATION: consensus Mig sequence
71 <400> SEQUENCE: 3
72 Thr Pro Val Val Arg Lys Gly Arg Cys Ser Cys Ile Ser Thr Asn Gln
73 1 5 10 15
74 Gly Thr Val His Leu Gln Ser Leu Glu Lys Leu Lys Ile Phe Ala Pro
75 20 25 30
76 Ser Pro Ser Cys Glu Lys Ile Glu Ile Ala Thr Leu Lys Lys Asn
77 35 40 45
78 Gly Val Gln Arg Cys Leu Asn Pro Asp Ser Lys Asp Val Lys Glu Leu
79 50 55 60
80 Ile Lys Lys Trp Glu Lys Gln Val Ser Gln Lys Lys Lys Gln Lys Asn
81 65 70 75 80
82 Gly Lys Lys His Gln Lys Lys Lys Val Leu Lys Val Arg Lys Val Gln
83 85 90 95
84 Arg Ser Arg Gln Lys Lys Thr Thr
85 100
88 <210> SEQ ID NO: 4
89 <211> LENGTH: 10
90 <212> TYPE: PRT
91 <213> ORGANISM: Artificial Sequence
93 <220> FEATURE:
94 <223> OTHER INFORMATION: epitope tag
96 <400> SEQUENCE: 4
97 Cys Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
98 1 5 10
101 <210> SEQ ID NO: 5
102 <211> LENGTH: 8
103 <212> TYPE: PRT
104 <213> ORGANISM: Artificial Sequence
106 <220> FEATURE:
107 <223> OTHER INFORMATION: epitope tag
109 <400> SEQUENCE: 5
110 Asp Tyr Lys Asp Asp Asp Asp Lys
111 1 5
114 <210> SEQ ID NO: 6
115 <211> LENGTH: 11
116 <212> TYPE: PRT
117 <213> ORGANISM: Artificial Sequence
119 <220> FEATURE:
120 <223> OTHER INFORMATION: epitope tag
122 <400> SEQUENCE: 6
123 Cys Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
124 1 5 10

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127 <210> SEQ ID NO: 7
128 <211> LENGTH: 5
129 <212> TYPE: PRT
130 <213> ORGANISM: Artificial Sequence
132 <220> FEATURE:
133 <223> OTHER INFORMATION: protease cleavage site
135 <400> SEQUENCE: 7
136 Asp Asp Asp Asp Lys
137 1 5
140 <210> SEQ ID NO: 8
141 <211> LENGTH: 4
142 <212> TYPE: PRT
143 <213> ORGANISM: Artificial Sequence
145 <220> FEATURE:
146 <223> OTHER INFORMATION: protease cleavage site
148 <400> SEQUENCE: 8
149 Ile Glu Gly Arg
150 1
153 <210> SEQ ID NO: 9
154 <211> LENGTH: 6
155 <212> TYPE: PRT
156 <213> ORGANISM: Artificial Sequence
158 <220> FEATURE:
159 <223> OTHER INFORMATION: protease cleavage site
161 <400> SEQUENCE: 9
162 Leu Val Pro Arg Gly Ser
163 1 5
166 <210> SEQ ID NO: 10
167 <211> LENGTH: 8
168 <212> TYPE: PRT
169 <213> ORGANISM: Artificial Sequence
171 <220> FEATURE:
172 <223> OTHER INFORMATION: protease cleavage site
174 <400> SEQUENCE: 10
175 His Pro Phe His Leu Val Ile His
176 1 5
179 <210> SEQ ID NO: 11
180 <211> LENGTH: 104
181 <212> TYPE: PRT
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Consensus Sequence for IP-10, I-TAC and Mig
W--> 187 <221> NAME/KEY: VARIANT
188 <222> LOCATION: 1, 3, 4, 6, 10, 14, 15, 16, 17, 18, 20, 21, 22, 28, 30, 31,
189 34, 35, 37, 50, 57, 60, 61, 63, 68, 69, 70, 71, 72, 73,
190 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87,
191 88, 89, 90, 91, 92, 93, 94, 96, 98, 99, 100, 103, 104
192 <223> OTHER INFORMATION: Xaa = Any Amino Acid
W--> 194 <400> 11

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```

W--> 195 Xaa Pro Xaa Xaa Arg Xaa Gly Arg Cys Xaa Cys Ile Ser Xaa Xaa Xaa
      196 1 5 10 15
      197 Xaa Xaa Val Xaa Xaa Xaa Ser Leu Glu Lys Leu Xaa Ile Xaa Xaa Pro
      198 20 25 30
      199 Ser Xaa Xaa Cys Xaa Lys Ile Glu Ile Ile Ala Thr Leu Lys Lys Asn
      200 35 40 45
      201 Gly Xaa Gln Arg Cys Leu Asn Pro Xaa Ser Lys Xaa Xaa Lys Xaa Leu
      202 50 55 60
      203 Ile Lys Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      204 65 70 75 80
      205 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa
      206 85 90 95
      207 Arg Xaa Xaa Xaa Lys Lys Xaa Xaa
      208 100
      211 <210> SEQ ID NO: 12
      212 <211> LENGTH: 98
      213 <212> TYPE: PRT
      214 <213> ORGANISM: Homo sapien
      216 <400> SEQUENCE: 12
      217 Met Asn Gln Thr Ala Ile Leu Ile Cys Cys Leu Ile Phe Leu Thr Leu
      218 1 5 10 15
      219 Ser Gly Ile Gln Gly Val Pro Leu Ser Arg Thr Val Arg Cys Thr Cys
      220 20 25 30
      221 Ile Ser Ile Ser Asn Gln Pro Val Asn Pro Arg Ser Leu Glu Lys Leu
      222 35 40 45
      223 Glu Ile Ile Pro Ala Ser Gln Phe Cys Pro Arg Val Glu Ile Ile Ala
      224 50 55 60
      225 Thr Met Lys Lys Lys Gly Glu Lys Arg Cys Leu Asn Pro Glu Ser Lys
      226 65 70 75 80
      227 Ala Ile Lys Asn Leu Leu Lys Ala Val Ser Lys Glu Met Ser Lys Arg
      228 85 90 95
      229 Ser Pro
      233 <210> SEQ ID NO: 13
      234 <211> LENGTH: 94
      235 <212> TYPE: PRT
      236 <213> ORGANISM: Homo sapien
      238 <400> SEQUENCE: 13
      239 Met Ser Val Lys Gly Met Ala Ile Ala Leu Ala Val Ile Leu Cys Ala
      240 1 5 10 15
      241 Thr Val Val Gln Gly Phe Pro Met Phe Lys Arg Gly Arg Cys Leu Cys
      242 20 25 30
      243 Ile Gly Pro Gly Val Lys Ala Val Lys Val Ala Asp Ile Glu Lys Ala
      244 35 40 45
      245 Ser Ile Met Tyr Pro Ser Asn Asn Cys Asp Lys Ile Glu Val Ile Ile
      246 50 55 60
      247 Thr Leu Lys Glu Asn Lys Gly Gln Arg Cys Leu Asn Pro Lys Ser Lys
      248 65 70 75 80
      249 Gln Ala Arg Leu Ile Ile Lys Lys Val Glu Arg Lys Asn Phe
      250 85 90

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Input Set : N:\efs\02_27_07\10555735a_efs\INTM01901USseqlist2.txt

Output Set: N:\CRF4\02272007\J555735A.raw

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253 <210> SEQ ID NO: 14
254 <211> LENGTH: 125
255 <212> TYPE: PRT
256 <213> ORGANISM: homo sapien
258 <400> SEQUENCE: 14
259 Met Lys Lys Ser Gly Val Leu Phe Leu Leu Gly Ile Ile Leu Leu Val
260 1 5 10 15
261 Leu Ile Gly Val Gln Gly Thr Pro Val Val Arg Lys Gly Arg Cys Ser
262 20 25 30
263 Cys Ile Ser Thr Asn Gln Gly Thr Ile His Leu Gln Ser Leu Lys Asp
264 35 40 45
265 Leu Lys Gln Phe Ala Pro Ser Pro Ser Cys Glu Lys Ile Glu Ile Ile
266 50 55 60
267 Ala Thr Leu Lys Asn Gly Val Gln Thr Cys Leu Asn Pro Asp Ser Ala
268 65 70 75 80
269 Asp Val Lys Glu Leu Ile Lys Lys Trp Glu Lys Gln Val Ser Gln Lys
270 85 90 95
271 Lys Lys Gln Lys Asn Gly Lys Lys His Gln Lys Lys Lys Val Leu Lys
272 100 105 110
273 Val Arg Lys Ser Gln Arg Ser Arg Gln Lys Lys Thr Thr
274 115 120 125
277 <210> SEQ ID NO: 15
278 <211> LENGTH: 98
279 <212> TYPE: PRT
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
283 <223> OTHER INFORMATION: hybrid CXCR3 ligand
285 <400> SEQUENCE: 15
286 Met Lys Lys Ser Gly Val Leu Phe Leu Leu Gly Ile Ile Leu Leu Val
287 1 5 10 15
288 Leu Ile Gly Val Gln Gly Phe Pro Met Phe Lys Arg Gly Arg Cys Leu
289 20 25 30
290 Cys Ile Gly Pro Gly Val Lys Pro Val Asn Pro Arg Ser Leu Glu Lys
291 35 40 45
292 Leu Glu Ile Ile Pro Ala Ser Gln Phe Cys Pro Arg Ile Glu Ile Ile
293 50 55 60
294 Ala Thr Leu Lys Asn Gly Val Gln Thr Cys Leu Asn Pro Asp Ser Lys
295 65 70 75 80
296 Gln Ala Arg Leu Ile Ile Lys Lys Val Ser Lys Glu Met Ser Lys Arg
297 85 90 95
298 Ser Pro
302 <210> SEQ ID NO: 16
303 <211> LENGTH: 124
304 <212> TYPE: PRT
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: hybrid CXCR3 ligand
310 <400> SEQUENCE: 16
311 Met Asn Gln Thr Ala Ile Leu Ile Cys Cys Leu Ile Phe Leu Thr Leu

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/555,735A

DATE: 02/27/2007
TIME: 15:05:51

Input Set : N:\efs\02_27_07\10555735a_efs\INTM01901USseqlist2.txt
Output Set: N:\CRF4\02272007\J555735A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. ~~1,3,4,6,10,14,15,16,17,18,20,21,22,28,30,31,34,35,37,50~~
Seq#:11; Xaa Pos. ~~57,60,61,63,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82~~
Seq#:11; Xaa Pos. ~~83,84,85,86,87,88,89,90,91,92,93,94,96,98,99,100,103,104~~

VERIFICATION SUMMARY

DATE: 02/27/2007

PATENT APPLICATION: US/10/555,735A

TIME: 15:05:51

Input Set : N:\efs\02_27_07\10555735a_efs\INTM01901USseqlist2.txt

Output Set: N:\CRF4\02272007\J555735A.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:187 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:194 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
M:341 Repeated in SeqNo=11